



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/889,053C
Source: 1699
Date Processed by STIC: 4/21/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

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MAY 24 2004

Raw Sequence Listing Error Summary

Technology Center 2600

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/889,053C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 _____ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
 Wrapped Aminos was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
 prevent "wrapping."
- 2 _____ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 _____ Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
 Numbering use space characters, instead.
- 4 _____ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
 ensure your subsequent submission is saved in ASCII text.
- 5 _____ Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules,
 each n or Xaa can only represent a single residue. Please present the maximum number of each
 residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 _____ PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
 "bug" sequences(s) _____. Normally, PatentIn would automatically generate this section from the
 previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
 the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
 Artificial or Unknown sequences.
- 7 _____ Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
 (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 _____ Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
 (NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 9 _____ Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
 (NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 _____ Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
 Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
 is Artificial Sequence
- 11 _____ Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
 "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 _____ PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
 "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
 listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 _____ Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

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AMC - Biotechnology Systems Branch - 09/09/2003

JUN 03 2004

TECHNOLOGY CENTER R3700



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RAW SEQUENCE LISTING

DATE: 04/21/2004

PATENT APPLICATION: US/09/889,053C

TIME: 07:53:27

Input Set : A:\7379P2rev.txt

Output Set: N:\CRF4\04212004\I889053C.raw

4 <110> APPLICANT: Keough, Thomas W.
 6 Youngquist, Robert S
 9 <120> TITLE OF INVENTION: Methods and Kits for Sequencing Polypeptides
 13 <130> FILE REFERENCE: Methods/Kits for Sequencing Polypeptid
 -> 17 <140> CURRENT APPLICATION NUMBER: US/09/889,053C
 19 <141> CURRENT FILING DATE: 2001-07-11
 23 <160> NUMBER OF SEQ ID NOS: 9
 27 <170> SOFTWARE: PatentIn Ver. 2.0

RORED SEQUENCES

31 <210> SEQ ID NO: 1
 33 <211> LENGTH: 8
 35 <212> TYPE: PRT
 37 <213> ORGANISM: synthetic construct
 41 <400> SEQUENCE: 1
 43 Ala Ser His Leu Gly Leu Ala Arg
 -> 45 1
 91 <210> SEQ ID NO: 4
 93 <211> LENGTH: 30
 95 <212> TYPE: PRT
 97 <213> ORGANISM: bovine
 101 <400> SEQUENCE: 4
 -> 103 Phe Val Asn Gln His Leu Cya Gly Ser His Leu Val Glu Ala Leu Tyr
 105 1 5 10 15
 -> 109 Leu Val Cya Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Ala
 111 20 25 30

invalid response - see item 10 on Error Summary Sheet

This error appears throughout

*Does Not Comply
Corrected Diskette Needed
Sequence Listing*

*Do not
use TAB
codes between amino
acid numbers.*

invalid amino acid designator

Use space characters.

*some
error*

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/889,053C

DATE: 04/21/2004

TIME: 07:53:28

Input Set : A:\7379P2rev.txt

Output Set: N:\CRF4\04212004\I889053C.raw

17 M:270 C: Current Application Number differs, Replaced Current Application Number

15 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1

103 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1

109 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1